## Amendments to the Claims

Claims 1-2 (Cancelled).

Claim 3 (Currently amended): A method of determining whether a compound modulates insulin receptor activity, comprising comparing using a processor all or part of the structure of the compound to all or part of the fitted quaternary structure of insulin receptor to determine whether the compound interacts with the insulin receptor, the comparing step comprising:

a) providing a computer program on the processor, the computer program including structural coordinates defining a ligand binding site conformation including at least one residue from monomer A in Table ~~I~~1 and at least one residue from monomer B in Table ~~I~~1, the ligand binding site defined by the approximate amino acid intersidechain distances listed in Table ~~I~~1, wherein the program displays the quaternary structure of the ligand binding site;

b) comparing the structural coordinates of the compound to the structural coordinates of the ligand binding site and determining whether the compound fits spatially into the ligand binding site ~~and is capable of changing insulin receptor from an inactive conformation to an active conformation or biasing insulin receptor toward an active conformation~~;

~~wherein the ability to change insulin receptor from an inactive conformation to an active conformation or bias insulin receptor toward an active conformation is predictive of the ability of the compound to modulate insulin receptor activity by agonizing insulin receptor activity~~

next determining whether the test compound modulates insulin receptor activity by determining if the test compound agonizes insulin receptor activity in an insulin receptor activity assay.

Claims 4-5 Cancelled

Claim 6 (Previously presented): The method of claim 3, wherein the fitted quaternary structure of insulin receptor comprises substantially the entire fitted quaternary structure of insulin receptor.

Claims 7-8 (Cancelled).

Claim 9 (Currently amended): A method of determining whether a compound modulates insulin receptor activity, comprising comparing using a processor all or part of the structure of the compound to all or part of the fitted quaternary structure of insulin receptor to determine how the compound interacts with the insulin receptor, the comparing step comprising:

a) providing a computer program on the processor, the computer program including structural coordinates defining a ligand binding site conformation including at least one residue from monomer A in Table ~~1~~ 1 and at least one residue from monomer B in Table 1, the ligand binding site defined by the approximate amino acid coordinates listed in Table 1, wherein the program displays the quaternary structure of the ligand binding site;

b) comparing the structural coordinates of the compound to the structural coordinates of the ligand binding site and determining whether the compound fits spatially into the ligand binding site ~~and is capable of changing insulin receptor from an active conformation to an inactive conformation or biasing insulin receptor toward an inactive conformation; wherein the ability to change insulin receptor from an active conformation to an inactive conformation or bias insulin receptor toward an inactive conformation is predictive of the ability of the compound to modulate insulin receptor activity by antagonizing insulin receptor activity;~~

next determining whether the test compound modulates insulin receptor activity by determining whether the test compound antagonizes insulin receptor activity in an insulin receptor activity assay.

Claim 10 (Cancelled).

Claim 11 (Currently amended): A method of determining whether a compound modulates insulin receptor activity, comprising comparing using a processor all or part of the structure of the compound to all or part of the fitted quaternary structure of insulin receptor to determine how the compound interacts with the insulin receptor, the comparing step comprising:

a) providing a computer program on the processor, the computer program including structural coordinates including at least one residue from between amino acids 250 to 280 of SEQ ID NO:16 ~~the Cam-loop segment in Table 2~~ and at least one residue from the L1 surface in Table 2, wherein the program displays the quaternary structure of the ligand binding site;

b) comparing the structural coordinates of the compound to the structural coordinates of ~~the~~ at least one residue between amino acids 250 to 280 of SEQ ID NO:16 ~~Cam-loop segment~~ and determining whether the compound interacts with the ~~Cam-loop segment~~ residue; ~~and is capable of changing insulin receptor from an inactive conformation to an active conformation or biasing insulin receptor toward an active conformation;~~

~~wherein the ability to change insulin receptor from an inactive conformation to an active conformation is predictive of the ability of the compound to modulate insulin receptor activity by agonizing insulin receptor activity~~

next determining whether the test compound modulates insulin receptor activity by determining whether the test compound agonizes insulin receptor activity in an insulin receptor activity assay.

Claim 12 (Cancelled).

Claim 13 (Currently amended): A method of determining whether a compound modulates insulin receptor activity, comprising comparing using a processor to compare all or part of the structure of the compound to all or part of the fitted quaternary structure of insulin receptor to determine how the compound interacts with the insulin receptor, the comparing step comprising:

a) providing a computer program on the processor, the computer program including structural coordinates ~~defining a cam conformation~~ including at least one residue between amino acids 250 to 280 of SEQ ID NO:16 ~~from the Cam-loop segment in Table 2~~ and at least one residue from the L1 surface in Table 2, wherein the program displays the quaternary structure thereof;

b) comparing the structural coordinates of the compound to the structural coordinates of the at least one residue between amino acids 250 to 280 of SEQ ID NO:16 ~~the Cam-loop segment~~ and determining whether the compound interacts with the ~~Cam-loop~~

~~segment~~residue; ~~and is capable of changing insulin receptor from an active conformation to an inactive conformation;~~

~~wherein the ability to change insulin receptor from an active conformation to an inactive conformation or bias insulin receptor toward an inactive conformation is predictive of the ability of the compound to modulate insulin receptor activity by antagonizing insulin receptor activity~~

next determining whether the test compound modulates insulin receptor activity by determining whether the test compound antagonizes insulin receptor activity in an insulin receptor activity assay.

Claim 14 (Cancelled).

Claim 15 (Previously presented): The method of claim 3, wherein the insulin receptor is bound to insulin.

Claims 16-19 (Cancelled).

Claim 20 (Previously presented): The method of claim 9, wherein the insulin receptor is bound to insulin.

Claim 21 (Previously presented): The method of claim 11, wherein the insulin receptor is bound to insulin.

Claim 22 (Previously presented): The method of claim 13, wherein the insulin receptor is bound to insulin.

Claim 23 (New): The method of claim 11, wherein the at least one residue between amino acids 250 to 280 of SEQ ID NO:16 comprises at least one residue selected from the group consisting of Lys265, Lys267, Asn268, Arg270, Arg271 and Gln272.

Claim 24 (New): The method of claim 13, wherein the at least one residue between amino acids 250 to 280 of SEQ ID NO:16 comprises at least one residue selected from the group consisting of Lys265, Lys267, Asn268, Arg270, Arg271 and Gln272.

Claim 25 (New): A method of determining whether a compound modulates insulin receptor activity, comprising comparing using a processor all or part of the structure of the compound to all or part of the fitted quaternary structure of insulin receptor or a derivative thereof to determine whether the compound interacts with the insulin receptor and will modulate insulin receptor activity.